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Fig. 1A

GACGCTTCTG GGGAGTGAGG GAAGCGGTTT ACAGTGACT TGGCTGGAGC CTCAGGGGCG GGCACCTGGCA CGGAACACAC  
 CCTGAGGCCA GCCCTGGCTG CCCAGGCGGA GCTGCCCTCTT CTCGCCGGGG TTGGTGGACC CGCTCAGTAC GGAGTTGGGG  
 AAGCTCTTC ACTTCGGAGG ATTGCTCAAC AACC 194

ATG CTG GGC ATC TGG ACC CTC CTA CCT CTG GTT CTT ACG TCT GTT GCT AGA TTA TCG TCC AAA AGT  
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala Arg Leu Ser Ser Lys Ser  
 -10 -1 1

GTT AAT GCC CAA GTG ACT GAC ATC AAC TCC AAG GGA TTG GAA TTG AGG AAG ACT GTT ACT ACA GTT  
 Val Asn Ala Gln Val Thr Asp Ile Asn Ser Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val  
 10 20

GAG ACT CAG AAC TTG GAA GGC CTG CAT GAT GGC CAA TTC TGC CAT AAG CCC TGT CCT CCA GGT  
 Glu Thr Gln Asn Leu Glu Gly Leu His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly  
 30 40 50

GAA AGG AAA GCT AGG GAC TGC ACA GTC AAT GGG GAT GAA CCA GAC TGC GTG CCC TGC CAA GAA GGG  
 Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly  
 60 70

AAG GAG TAC ACA GAC AAA GCC CAT TTT TCT TCC AAA TGC AGA AGA TGT AGA TTG TGT GAT GAA GGA  
 Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly  
 80 90

CAT GGC TTA GAA GTG GAA ATA AAC TGC ACC CGG ACC CAG AAT ACC AAG TGC AGA TGT AAA CCA AAC  
 His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro Asn  
 100 110

TTT TTT TGT AAC TCT ACT GTA TGT GAA CAC TGT GAC CCT TGC ACC AAA TGT GAA CAT GGA ATC ATC  
 Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile  
 \*120 130

Fig. 1B

AAG GAA TGC ACA CTC ACC AGC AAC ACC AAG TGC AAA GAG GAA GGA TCC AGA TCT AAC TTG GGG TGG	
Lys Glu Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys	150
	160
CTT TGT CTT CTT CTT TTG CCA ATT CCA CTA ATT GTT TGG GTG AAG ACG AAG GAA GTA CAG AAA ACA	
Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val Gln Lys Thr	180
	170
TGC AGA AAG CAC AGA AAG GAA AAC CAA GGT TCT CAT GAA TCT CCA ACC TTA AAT CCT GAA ACA GTG	
Cys Arg Lys Lys His Arg Lys Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val	200
	190
GCA ATA AAT TTA TCT GAT GTT GAC TTG AGT AAA TAT ATC ACC ACT ATT GCT GGA GTC ATG ACA CTA	
Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Thr Ile Ala Gly Val Met Thr Leu	220
	210
AGT CAA GTT AAA GGC TTT GTT CGA AAG AAT GGT GTC AAT GAA GCC AAT ATA GAT GAG ATC AAG AAT	
Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn	240
	230
GAC AAT GTC CAA GAC ACA GCA GAA CAG AAA GTT CAA CTC CTT CGT AAT TGG CAT CAA CTT CAT GGA	
Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly	270
	250
AAG AAA GAA GCG TAT GAC ACA TTG ATT AAA GAT CTC AAA AAA	
Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys	280

Fig. 2A

1100  
GCC AAT CTT TGT ACT CTT GCA GAG AAA ATT CAG ACT ATC ATC CTC AAG GAC ATT ACT AGT GAC TCA  
Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser  
290 300 1150

GAA AAT TCA AAC TTC AGA AAT GAA ATC CAA AGC TTG GTC TAG AGTGAAAAACAACAATTTCAGTTCTGA  
Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val End  
310 319 1200

1250 1300  
GTATATGCAATTAGTGTGTTGAAAAGATTCTTAATAGCTGGCTGTAAATACTGCTTGGTTTTTTTACTGGGTACATTTTATC  
1350  
ATTTATTAGCGCTGAAGAGCCACATATTTGTAGATTTTAAATATCTCATGATTTGCTCCCAAGGATGTTTAAAAATCTA  
1400 1450  
GTTGGGAAAACAACAACTTCATCAAGAGTAAATGCAGTGGCATGCTAAGTACCCAAATAGGAGTGTATGCAGAGGATGAAAG  
1500 1550  
ATTAAGATTATGCTCTGGCATCTAACATATGATTTCTGTAGTATGAATGTAATCAGTGTATGTTAGTACAAATGTCTATCC  
1600  
ACAGGCTAACCCCACTCTATGAATCAATAGAGAAGCTATGACCTTTTGCTGAAATATCAGTTACTGAACAGGCAGGCCA  
1650 1700  
CTTTGCCCTCTAAATTACCTCTGATAATTCTAGAGATTTTACCATAATTCTAAACTTTGTTTATACTCTGAGAAGATCAT  
1750  
ATTTATGTAAGTATATGATTTGAGTGCAGAAATTTAAATAAGGCTCTACCTCAAGACCTTTCACACAGTTTATTGGTGT

Fig. 2B

1800  
 1850  
 1900  
 1950  
 2000  
 2050  
 2100  
 2150  
 2200  
 2250  
 2300  
 2350  
 2400  
 2450  
 TACGTAATTAATAATGTTTTG

TATTATACAATATTCAATTGTGAATTCACATAGAAAACATTAAATTTAAATGTTTGACTATTATATATATGTGTATGCA  
 TTAGCTGGCTCAAAACTACCTACTTCTTCTCAGGCATCAAAAGCATTTTGAGCAGGAGAGTATTACTAGAGCTTTTGCC  
 CTCTCCATTTTGCCTTGGTGCTCATCTTAATGGCCTAATGCACCCCAACATGGAATATCACCACAAAATACTTA  
 AGTCCACCAAAAGGCAAGACTGCCCTTAGAAAATTCTAGCCTGGTTTGGAGATACTAACTGCTCTCAGAGAAAGTAGCT  
 CTGACATGTCAAGACCCCATGTTTGCAATCAAAAGATGATAAAATAGATTCTTATTTTCCCCCACCACCCGAAATGTT  
 ATAATGTCCCATGTAAAACCTGCTACAAAATGGCAGCTTATACATAGCAATGGTAAATCATCATCTGGATTTAGGAAAT  
 CTCTTGTCATACCCCTCAAGTTTCTAAAGATTAAAGATTCTCCTTACTACTATCCTACGTTTAAATATCTTTGAAGTTT  
 ATTAATGTGAATTTAAGAAAATAATTTATATTTCTGTAAATGTAAACTGTGAAGATAGTTATAAACTGAAGCAGA  
 CCTGGAACCACTAAAGAACTTCCATTTATGGAGGATTTTTTTTGCCCCCTTGTGTTTGGAAATTATAAAATATAGGTAAA  
 TACGTAATTAATAATGTTTTG

FIG 3A

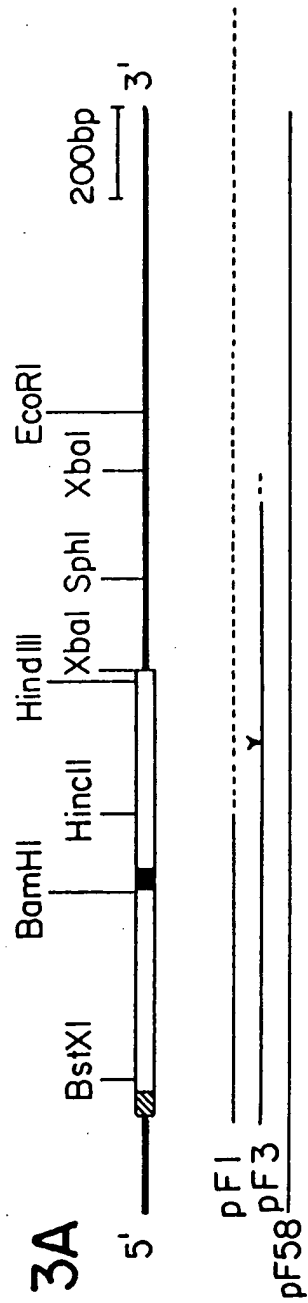


FIG 3B

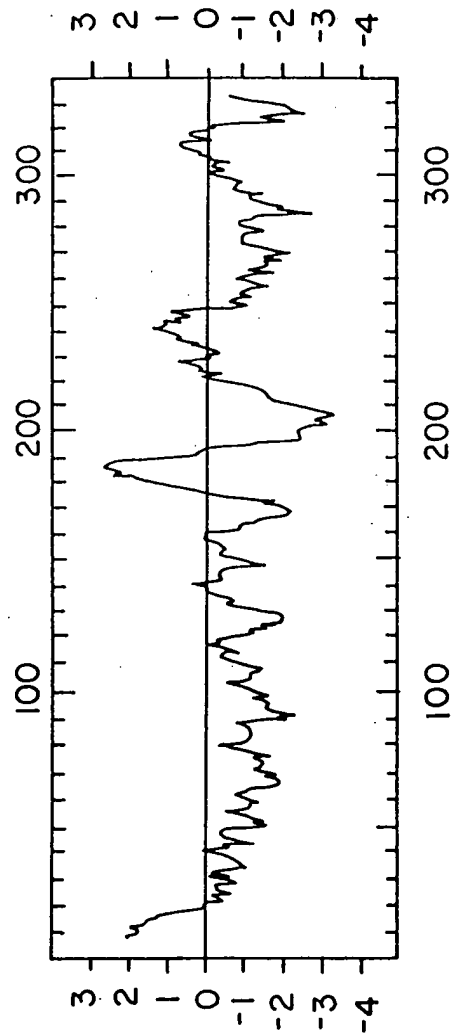


FIG.4A

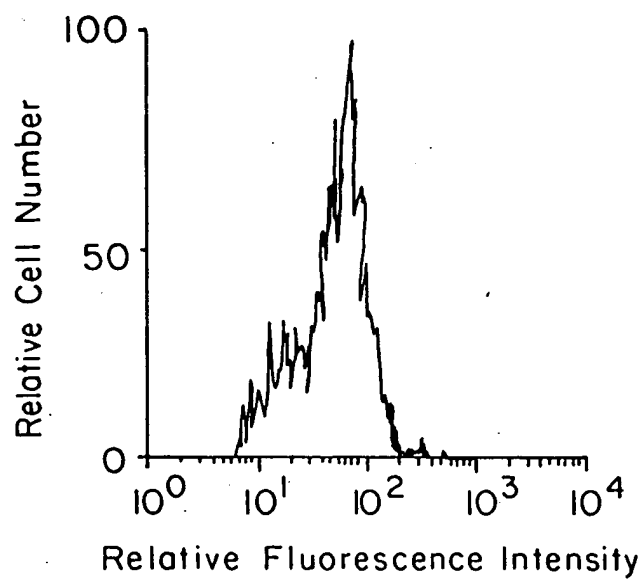
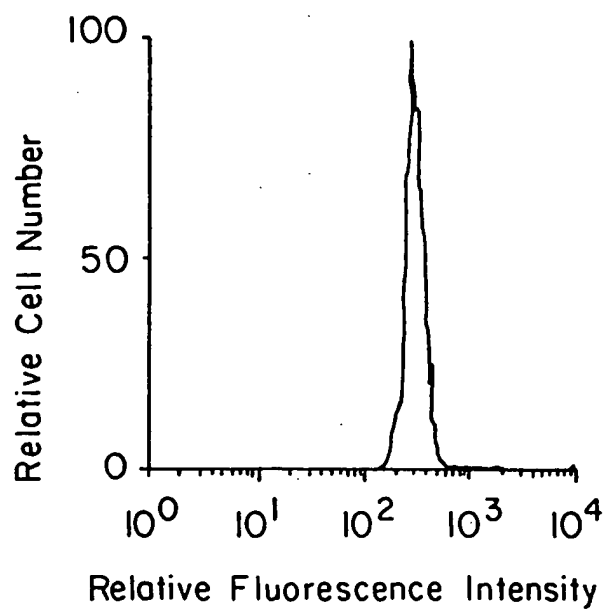


FIG.4B



09884987-062101  
TOT290-864860

FIG. 4C

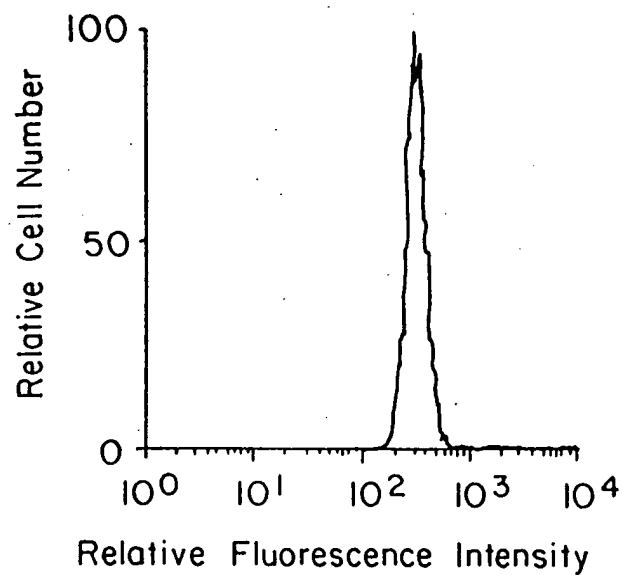


FIG. 4D

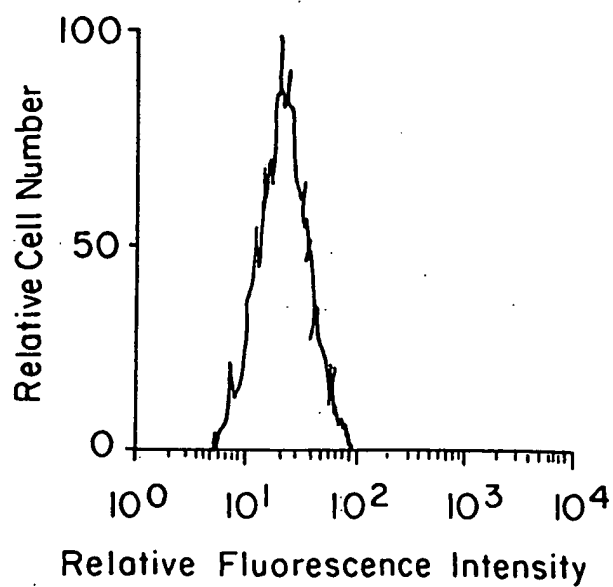




FIG. 4E

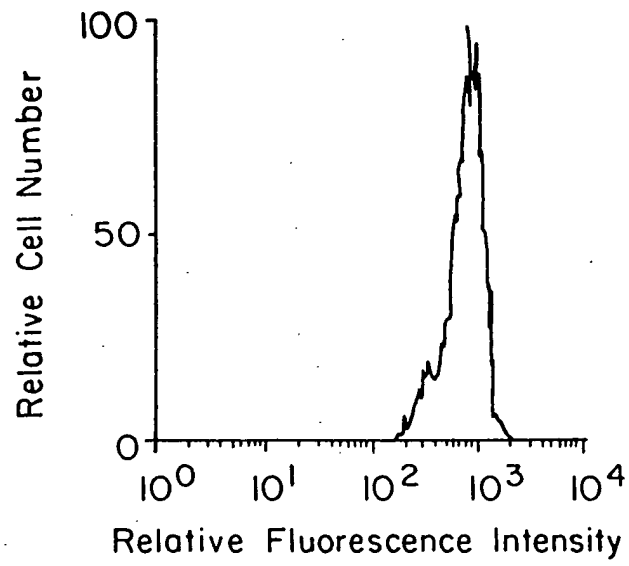


FIG. 4F

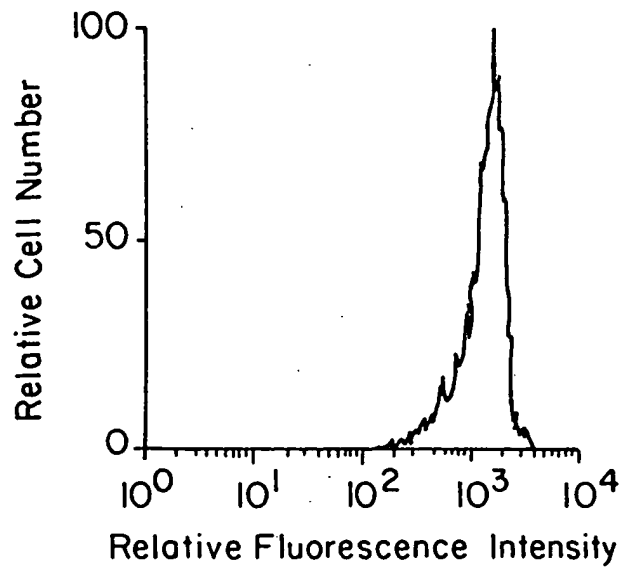


FIG. 5

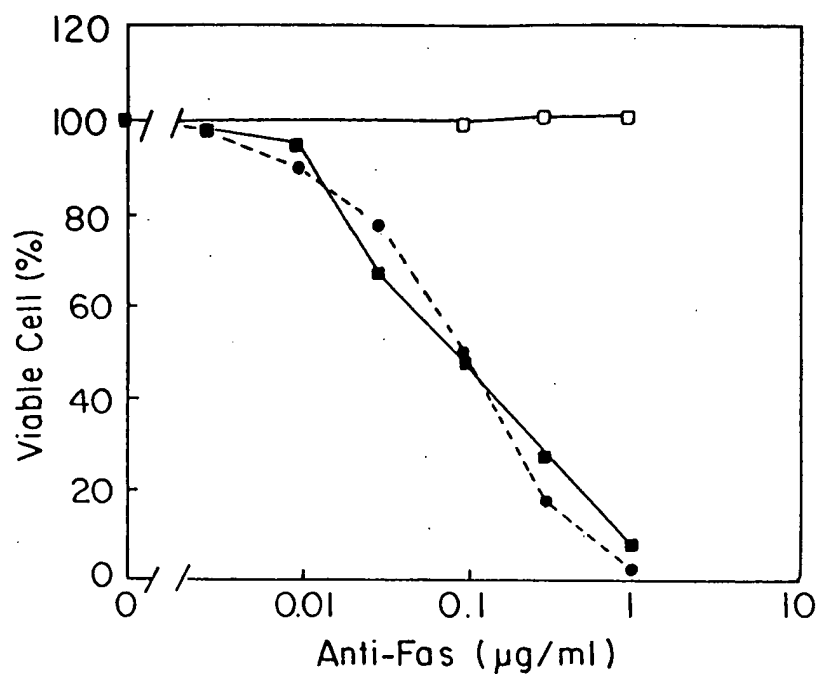


FIG. 6

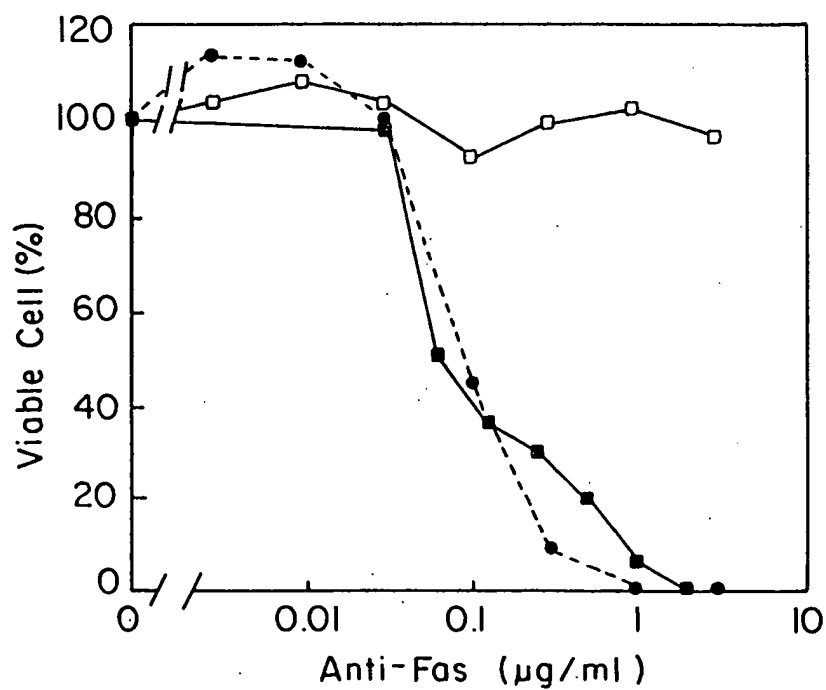
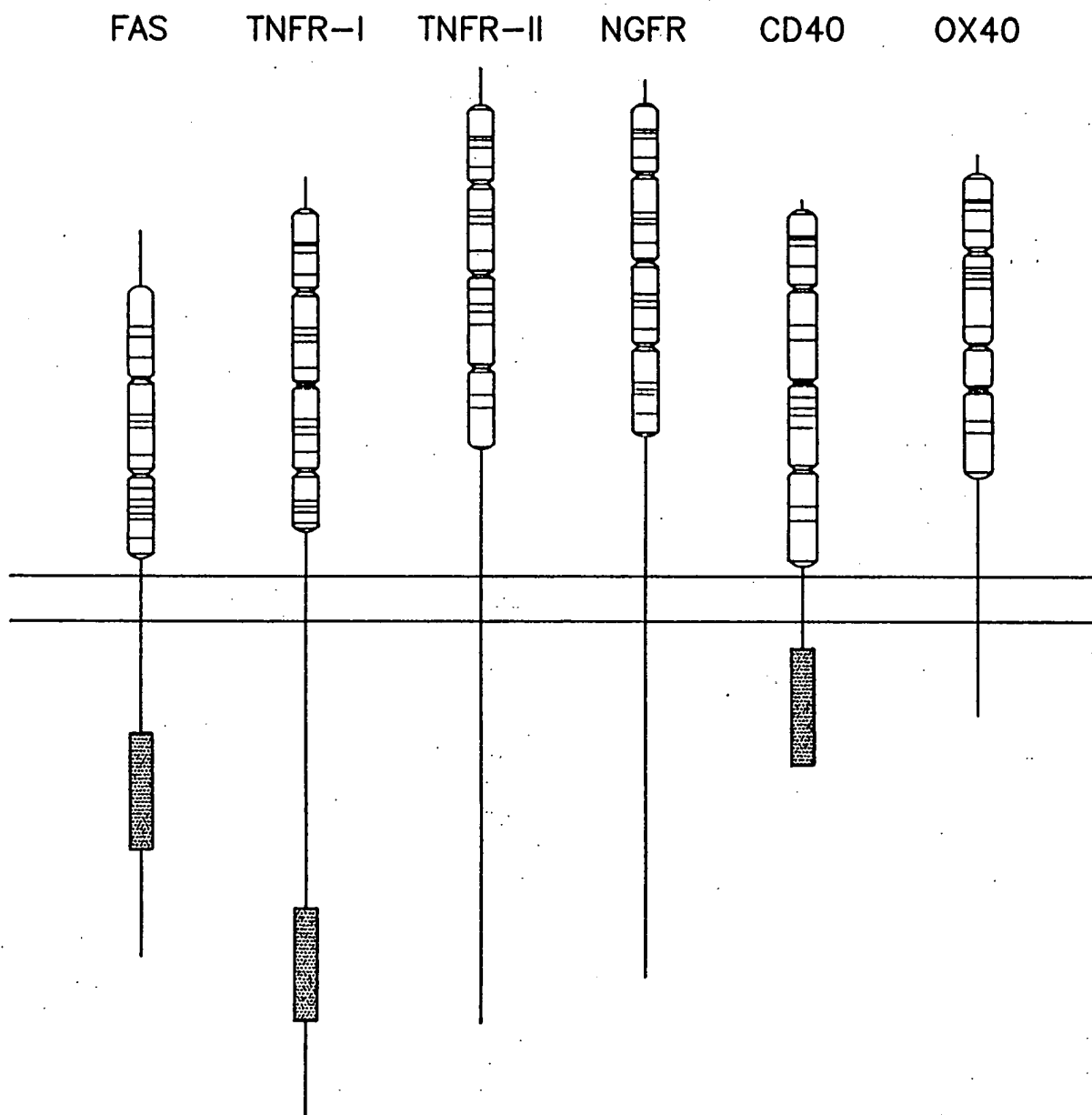


FIG. 7



hFAS (31-67)	K	T	S	K	S	R	R	S	S	T	K	T	-	-	P	-	L	-	S	Q	T	T	T
hTNR1 (3-42)	-	-	-	-	-	-	-	-	G	-	-	-	-	-	A	-	V	-	-	-	-	-	
hTNR2 (39-76)	H	C	C	C	C	C	C	C	C	C	C	H	C	C	C	C	C	-	C	H	C	-	W
hNGFR (3-37)	C	C	C	C	C	C	R	S	S	P	Q	Q	P	N	L	A	S	-	S	P	P	P	P
hCD40 (25-60)	-	I	M	-	-	-	R	L	L	K	H	K	D	F	R	E	E	-	V	R	L	H	K
roX40 (25-60)	-	S	Q	-	-	-	C	C	C	C	C	C	C	C	C	C	C	-	C	C	C	C	C
hFAS (68-112)	-	-	-	-	-	-	K	H	E	P	-	T	H	Q	G	R	A	S	-	I	P	K	A
hTNR1 (43-86)	-	-	-	-	-	-	S	R	P	E	E	C	E	E	E	S	E	C	-	C	C	E	-
hTNR2 (77-119)	-	-	-	-	-	-	S	-	-	-	-	-	C	-	C	-	S	C	-	-	-	-	-
hNGFR (38-80)	-	-	-	-	-	-	F	L	V	A	E	Y	V	N	K	T	T	R	E	T	V	F	-
hCD40 (61-104)	F	N	A	-	-	-	H	H	W	S	R	N	T	E	S	E	-	-	N	S	H	A	Q
roX40 (61-103)	Q	N	T	E	Q	K	A	N	N	V	N	V	S	S	L	-	-	-	E	S	N	S	N
hFAS (113-149)	G	Q	Q	G	S	H	K	E	W	V	W	A	-	W	-	-	-	-	-	T	A	S	S
hTNR1 (87-126)	D	P	-	S	N	G	D	S	L	D	T	E	-	Y	-	-	-	-	-	T	E	V	G
hTNR2 (120-162)	H	H	D	H	I	S	T	A	Q	S	D	N	N	H	A	D	-	-	R	N	D	N	P
hNGFR (81-119)	-	I	Y	T	L	P	Y	T	T	S	L	Y	C	R	C	Q	C	P	L	S	S	S	S
hCD40 (105-144)	H	Y	Y	Y	Y	Y	E	F	Y	T	F	F	F	Y	Y	Y	H	Q	F	F	Y	F	F
roX40 (104-123)	L	K	E	L	Q	T	K	S	T	V	E	G	F	Q	W	Y	W	T	F	T	T	F	H
hTNR1 (127-155)	G	G	R	G	K	D	G	G	S	S	S	P	N	N	G	G	G	G	G	G	G	G	G
hTNR2 (163-201)	E	Q	L	T	E	K	E	S	D	D	E	E	P	K	P	Y	E	P	A	P	D	V	P
hNGFR (120-161)	L	P	R	P	R	V	Q	E	E	L	G	-	K	R	R	A	E	R	H	A	P	P	P
hCD40 (145-186)	N	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
roX40 (124-164)	Q	V	T	A	A	N	P	E	S	P	P	P	-	-	-	-	-	-	T	P	E	P	P
Consensus																							

Fig. 813

V	R	D	E	L	H	R	G	T	R	T	Q	-	-	K	E	E	V	-	T	E	G	E	
C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
D	D	V	V	E	V	K	V	I	V	I	V	K	V	V	V	I	-	L	V	E	V	V	V
P	T	T	T	T	T	T	T	R	A	T	T	T	T	V	T	T	-	-	A	A	V	T	T
E	D	D	Q	E	D	N	D	N	D	D	D	N	N	D	N	D	-	-	D	D	D	D	D
D	Q	-	N	T	R	Q	R	Q	D	T	E	S	Q	S	Q	S	-	-	M	A	T	L	
G	G	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	K	S	
N	P	T	-	F	T	T	D	E	A	E	T	T	K	T	K	V	-	-	A	W	N	N	
V	G	K	A	E	H	R	V	R	E	S	P	L	E	E	D	G	-	K	N	R	T	S	
T	P	T	G	T	D	T	T	T	V	T	T	T	Q	T	Q	T	-	T	G	T	G	A	T
C	C	C	C	C	C	C	C	C	C	G	C	C	C	G	C	E	-	C	P	C	A	P	C
-	-	-	-	-	-	N	S	A	-	K	N	-	S	P	S	I	-	E	I	E	Q	H	
-	-	-	-	-	-	I	S	Q	-	Q	Q	E	L	R	F	Q	-	-	-	-	-	-	
D	D	F	P	D	R	E	I	T	P	Q	K	K	H	A	V	K	D	-	-	-	-	-	
R	N	V	Q	S	S	V	E	E	A	V	L	I	V	V	L	V	V	-	A	R	Q	R	
A	Y	K	A	V	V	E	V	V	S	R	E	-	-	G	G	G	G	-	V	L	V	I	
K	L	A	V	L	M	L	Q	Q	M	L	S	I	T	F	S	F	F	-	V	Q	V	Q	
R	Y	H	G	K	G	G	G	-	S	G	G	G	G	G	G	G	K	-	-	R	L	K	
E	T	Q	E	Q	H	H	M	-	Q	L	S	H	N	P	A	P	H	L	-	E	D	G	
G	G	G	G	G	G	G	E	D	L	N	R	E	L	R	E	S	S	S	-	T	K	S	
P	K	P	L	P	P	E	K	D	G	P	H	C	C	C	C	C	-	K	-	D	T	L	
P	H	S	N	Q	Q	D	R	S	V	D	N	K	L	K	V	S	-	K	N	E	E	T	
C	C	C	C	C	C	C	C	C	C	C	C	T	S	R	R	R	-	C	C	C	C	C	C
P	K	K	A	L	E	L	K	R	E	Y	Q	-	-	L	-	H	-	N	I	V	S	N	

Fig 9

CD40 (225-247)	K	A	P	H	P	K	Q	E	P	Q	E	I	N	F	D	D	L	P	G	S	N	T
FAS (230-251)	K	G	F	V	R	K	N	G	V	N	E	A	K	I	D	E	I	K	N	D	N	V
TNFR1 (332-353)	K	E	F	V	R	R	L	G	L	S	D	H	E	I	D	R	L	E	L	Q	N	G
CD40 (248-269)	A	A	P	V	Q	E	T	L	H	G	C	Q	P	V	Q	E	D	G	-	K	E	S
FAS (252-274)	Q	D	T	A	E	Q	K	V	Q	L	L	R	N	W	Q	L	H	G	K	K	E	A
TNFR1 (354-376)	R	C	L	R	E	A	Q	Y	S	M	L	A	T	W	R	R	T	P	R	R	E	A